

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 20:58:41 ; Search time 1527.5 Seconds  
(without alignments)  
16168.980 Million cell updates/sec

Title: US-10-025-514-7

Perfect score: 1525

Sequence: 1 tctagaccatgctgaaag.....ccaactcagaagtagtcgac 1525

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	433.2	28.4	2478	11	AF130068
2	431.6	28.3	2571	11	AF113676
3	331.6	21.7	1392	11	AK002537
4	318.8	20.9	1296	11	AK004999
5	309.8	20.3	887	14	BQ643710
6	305.4	20.0	907	14	BQ648909

7	289.6	19.0	895	14	BQ653587	AGENCOURT
8	287	18.8	985	14	BM924019	AGENCOURT
9	285.2	18.7	982	14	BQ646142	AGENCOURT
10	283.8	18.6	924	14	BQ958958	AGENCOURT
11	274.8	18.0	1194	14	BM924813	AGENCOURT
12	273.4	17.9	907	14	BQ650189	AGENCOURT
13	271.4	17.8	891	14	BQ646948	AGENCOURT
14	270.4	17.7	959	14	BQ648524	AGENCOURT
15	268	17.6	796	12	BQ567260	AGENCOURT
16	264.8	17.4	833	14	BQ007663	UI-H-EIO-
17	264.8	17.4	991	14	BQ064738	AGENCOURT
18	263.8	17.3	917	14	BQ650502	AGENCOURT
19	263.6	17.3	687	10	AV649258	AV649258
20	263	17.2	916	14	BQ644130	AGENCOURT
21	262	17.2	686	12	BQ569467	AGENCOURT
22	261	17.1	1012	14	BQ064473	AGENCOURT
23	260.2	17.1	977	14	BQ654015	AGENCOURT
24	259.6	17.0	740	10	AV653778	AV653778
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27	254	16.7	917	14	BQ650698	AGENCOURT
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## ALIGNMENTS

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LOCUS  
DEFINITION Homo sapiens clone FLB8226 PRO2209 mRNA, complete cds.  
ACCESSION AF130068  
VERSION AF130068.1 GI:11493442  
KEYWORDS HTC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2478)  
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y., Xu, W., Gao, F., Liu, M. and He, F.  
TITLE Functional prediction of the coding sequences of 75 new genes deduced by analysis of cDNA clones from human fetal liver  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2478)  
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y., Xu, W., Gao, F., Liu, M. and He, F.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China  
FEATURES  
source Location/Qualifiers  
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/clone="FLB8226"









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Best Local Similarity 55.6%; Pred. NO. 1.7e-71;
Matches 655; Conservative 0; Mismatches 517; Indels 6; Gaps 2;

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DB 113 TCTGGGTGAGGATGTTCAAGGACACACACCTCCAGAGGATCAGTCC--CCAGCCTC 169
QY 404 TAATAAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTTGTATAGACAATAGCTCA 463
DB 170 CCATGAGATTGCTACAAACCTGGGAGACTTTGCCATCAGTCTATACCGGGAGCTGGTCCA 229
QY 464 TCAAGTAATTTACTACAACTTTTATTTAGTCTGCTTTTCTATTTGACCTGCTTTCCGCCAT 523
DB 230 TCAGTCAACACACTTCCAACTCTCTCTCCCGAGTGAGCATTTGCCACGCTTTGCTAT 289
QY 524 GTTGAGTTTAGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAACTTTAA 583
DB 290 GCTCTCCCTAGGAGCAGGAGTGCACACTCACCGCAGATCTTAGAGGCGCTGCAGTTCAA 349
QY 584 TTTGACCGAAATCCCAAGCCCAATTCACGAGGTTTTCACAGAGTGTGTGAGAACTTT 643
DB 350 CCTCACACAAACATCGGAGGTGACATCCCAATTCCTCCACACACTCTCTGCAACAATGA 469
QY 644 GAATCAACCTGATCTCAATTTGCAATTAATCTAGTGAAGGTTTATTTTGTCTGAAGG 703
DB 410 CAACAGACCCAGACAGTACGCTGACGTCAGCAGCAGCAATGGCTCTCTGCAACAATGA 469
QY 704 TTTAAATTTGTTGACAAATTTCTTAGAAGAGCTCAAGAACTATATCATAGTACGCTTT 763
DB 470 CTTGAGCTGTTGGGAGAAGTTCTTGAAGAGGCAAGCAATATCAGCAGCAAGTCTT 529
QY 764 TACCGTTAATTTTGTGTACTAGGAGCTTAAAGCAATTAATGATTTATGTATGTAGAA 823
DB 530 CTTCTGTCACTTTGAGAGTCAAGGAGGCGCAAGAAAGTATTAATGATTTTGTGGAGAA 589
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DB 590 GGAACCCAGGAAAGATAGTTGAGGCTGTGAAAAAACTAGAACAGACACAGTTTTCGT 649
QY 884 ACTGATTAATATATATTTTCAAGGGTAAGTGGGAAGCTCTCTTCCAGGTTTAAAGATAC 943
DB 650 CTTGGCAATTTACATTTCTTTTAAAGGCAATGGGAAGGCAATTCGATCTCTGAGACAC 709
QY 944 TGAAGAGGAGAGATTTTCATGTTGATCAAGTTACTACTGTCAAAAGTTCCAAATGATGAAAG 1003

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Db 710 TAAGCAAGCTGAGTTCACGTGACGAGTCCACCAGGTGAAGTGCCTATGACCT 769
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QY 1064 GTATTTAGGTAAGCTACTGCTATTTTATTTTACAGAGGAGTAAGCTTCAACATTT 1123
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QY 1304 AG---AAGCTCCATTTAAATTTAGTAAAGTGTTCACAAAGCCGCTTAACTTATGATGA 1360
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RESULT 5
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LOCUS AGENCOURT_8342217 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6268225
DEFINITION 5', mRNA sequence.
ACCESSION BQ643710
VERSION BQ643710.1 GI:21767882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Published: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LICM2439 row: n column: 02
High quality sequence stop: 731.
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ECORI; cDNA made by oligo-dr priming. Directionally cloned  
into EcorI/XhoI sites using the following 5' adaptor:  
GCCACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."  
BASE COUNT 242 a 224 c 232 g 187 t 2 others  
ORIGIN

Query Match 20.3%; Score 309.8; DB 14; Length 887;  
Best Local Similarity 60.0%; Pred. No. 3.1e-69;  
Matches 532; Conservative 0; Mismatches 354; Indels 1; Gaps 1;  
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DEFINITION B0648909.1 GI:21773081  
ACCESSION B0648909  
VERSION B0648909.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 907)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: CGAP (Stanford)  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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ECORI; cDNA made by oligo-dr priming. Directionally cloned  
into EcorI/XhoI sites using the following 5' adaptor:  
GCCACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

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Query Match 20.0%; Score 305.4; DB 14; Length 907;  
Best Local Similarity 59.8%; Pred. No. 4.4e-68;  
Matches 530; Conservative 0; Mismatches 356; Indels 1; Gaps 1;  
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RESULT 8
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ACCESSION BM924019
VERSION BM924019.1 GI:19374398
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 985)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12806 row: m column: 16
High quality sequence stop: 707.
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female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Matches 519; Conservative 0; Mismatches 351; Indels 2; Gaps 2;

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Db 174 CCAAGCTGCTGAGTTCGCTTACCGCTATATACCGCTGATGATGATGATGATGATGATG 233
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QY 958 TTCATGTTGATCAAGTACTACTGTCGTAAGTTCCTCAATGATGATGATGATGATGATGAT 1017
Db 714 TCCAGTGGACAGGTGACCAACCGTGAAGTGCCTATGATGAAGCGTTTTCAGCATGTTA 773
QY 1018 ATATTCACATTTGCAAAAATTAAGTTCTTGGGCTTTAATTAAGTGAATTTAGTAAAG 1077
Db 774 ACATCCAGCACTGTAAGAGCTGTTCCAGCTGGGTGCTGCTGATGAATACCTGGGCAATG 833
QY 1078 CTACTGCTAT-TTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTTAGAGAAATGATTG 1136
Db 834 CCACCGCCATCTTCTTCNTGGCTGATGAGGGGAAACTACAGGCACTGGAATAATCACTC 893
QY 1137 ACTCATGACATTTATTAATTTTATTTTAGAGAA 1168
Db 894 AC-CAGATATCATCAAGGTTCTCTGGAAA 924

RESULT 9
BQ646142
LOCUS BQ646142
DEFINITION 982 bp mRNA linear EST 15-JUL-2002
ACCESSION BQ646142
VERSION BQ646142.1 GI:21770314
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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QY 708 AAATGTTGTTGACAAATTCCTAGACAGCTCAAGAACTATATCATAGTAGGCTTTTACC 767
Db 302 AACCTAGTGATGAATGTTTGGAGATGTTAAAAAGTTTACCACTCAGAACGCTTCACT 361
QY 768 GTTAATTTTGGTACTACTGAGGAAGCTAAAAAGCAAAATTAATGATTATGTTGAGAAAGGC 827
Db 362 GTCAACTTCGGGACACCGGAGCCAGAAACAGATCAACGATTACGCTGGAGAGGCT 421
QY 828 ACCAGGGTAAAGATGTTGACCTAGCTTAAAGAAATAGATCTGATACCGCTTTCGCACTA 887
Db 422 ACTCAAGGAAATTTGTGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTCCTCTG 481
QY 888 GTTAATTAATTTTCAAGGGTAAGTGGGAAGCTCTCTTTCGAGGTTAAAGATACATGAA 947
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5', mRNA sequence.
BM924813
VERSION
KEYWORDS
SOURCE
EST.
BM924813.1 GI:19375192
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Best Local Similarity 61.2%; Pred. No. 4e-60;
Matches 444; Conservative 0; Mismatches 282; Indels 0; Gaps 0;
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QY 892 ACTATATTTTTCAGGGTAAGTGGGAAGCTCTTTCAGAGTTAAAGATCTGGAAGAGG 951
Db 127 ATTACATCTCTTTAAGGCAATATGGGAGAGACCCCTTTGAAGTCAAGGACACCGGAAG 186
QY 952 AAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTTCAATGATGAAGAACTGGGTA 1011
Db 187 AGSACTTCCAGCTGGACCAAGTCAACCCGTGAAGTGGCTATGATGAAGCGTTTAGGCA 246
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Db 247 TGTTAATCCACGACTGTAAAGCTGTCCAGCTGGGTGCTGTGATGAATACCTGG 306
QY 1072 GTACGCTACTGCTATTTTATTTTACCAGACGAAGCTTAAGCTTCAACATTTTAGAATG 1131
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Mon Dec 9 12:50:59 2002

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RESULT 12
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DEFINITION 5', mRNA sequence.
ACCESSION BQ650189
VERSION BQ650189.1 GI:21774361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 907)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2443 row: g column: 22
High quality sequence stop: 650.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOT7; Site: 1; XhoI; Site 2:
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 245 a 237 c 226 g 198 t 1 others
ORIGIN
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Best Local Similarity 59.4; Pred. No. 8.4e-60;
Matches 498; Conservative 0; Mismatches 337; Indels 3; Gaps 2;

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QY 720 AAATTCCTAGAGAGCTCAAGAACTATATCATAGTAGGCGTTTACCGTTAATTTTGGT 779
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QY 780 GATACGAGGAGCTTAAAGCAATTAATGATTATGTTGAGAAGGCAAGGCGGTAAG 839
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QY 1380 GGGCTATGCTCTGGAAGCTATTCATGAGCTATCCAGGAGTTCAGGCGGCTAGGTAT 1437
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QY 1438 AACCATTCGTTTCTGATGATCGAGAGCAACACTAAAGCGGCTAGGTATTTGGTAA 1495
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RESULT 13
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LOCUS AGENCOURT_8302495 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271313
DEFINITION 5', mRNA sequence.
ACCESSION BQ646948
VERSION BQ646948.1 GI:21771120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2447 row: n column: 18
High quality sequence stop: 672.
Location/Qualifiers
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Mon Dec 9 12:50:59 2002

us-10-025-514-7\_1.rst

Page 15

Search completed: December 6, 2002, 23:32:54  
Job time : 1546.5 secs



